from
US 10/780, 703-2.p2N.rnpm   *Seq Serdch Result*

(Seq 3) does Not encode Seq 2

```
RESULT 10
US-10-780-703-3
; Sequence 3, Application US/10780703
; GENERAL INFORMATION:
;   APPLICANT: Lee, Jong Seob
;   APPLICANT:  Kim, Yun Hee
;   APPLICANT:  Choi, Eun kyung
;   APPLICANT:  Yoo, So Yeon
;   APPLICANT:  Ahn, Ji Hoon
;   APPLICANT:  Choi, Yang Do
;   TITLE OF INVENTION: Gene Controlling Flowering Time of Plants and Method for
;   TITLE OF INVENTION:  Manipulating Flowering Time of Plant Using the Same
;   FILE REFERENCE: 012679-105
;   CURRENT APPLICATION NUMBER: US/10/780,703
;   CURRENT FILING DATE:  2004-02-19
;   PRIOR APPLICATION NUMBER: KR 10-2003-10772
;   PRIOR FILING DATE: 2003-02-20
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 2606
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)...(2606)
;   OTHER INFORMATION: genomic DNA of LOV1 gene
US-10-780-703-3
```

Alignment Scores:

Pred. No.:	1.24e-254	Length:	2606
Score:	1735.00	Matches:	378
Percent Similarity:	43.5%	Conservative:	0
Best Local Similarity:	43.5%	Mismatches:	1
Query Match:	85.3%	Indels:	490
DB:	61	Gaps:	3

US-10-780-703-2 (1-379) x US-10-780-703-3 (1-2606)

```
Qy        1 MetAlaIleValSerSerThrThrSerIleIleProMetSerAsnGlnValAsnAsnAsn 20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGCAATTGTATCCTCCACAACAAGCATCATTCCCATGAGTAACCAAGTCAACAATAAC 60

Qy       21 GluLysGlyIleGluAspAsnAspHisArgGlyGlyGlnGluSerHisValGlnAsnGlu 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 GAAAAAGGTATAGAAGACAATGATCATAGAGGCGGCCAAGAGAGTCATGTCCAAAATGAA 120

Qy       41 AspGluAlaAspAspHisAspHisAspMetValMetProGlyPheArgPheHisProThr 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GATGAAGCTGATGATCATGATCATGACATGGTCATGCCCGGATTTAGATTCCATCCTACC 180

Qy       61 GluGluGluLeuIleGluPheTyrLeuArgArgLysValGluGlyLysArgPheAsnVal 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAAGAAGAACTCATAGAGTTTTACCTTCGCCGAAAAGTTGAAGGCAAACGCTTTAATGTA 240

Qy       81 GluLeuIleThrPheLeuAspLeuTyrArgTyrAspProTrpGluLeuPro--------- 97
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GAACTCATCACTTTCCTCGATCTTTATCGCTATGATCCTTGGGAACTTCCTGGTAAATAT 300

Qy       97 ----------------------------------------------------------- 97
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Db    301 ACATTCACATAAACACACATAAATCATCTCAAACTATTTGGAAATCTTAATTTCTATTCA 360

Qy     97 ---------------------------------------------------------- 97

Db    361 TATGTTAAGATCTTTCTTCTCTCTTATCACTTTCTCTCTCTATTTCTTTTTTTTTAACCT 420

Qy     97 ---------------------------------------------------------- 97

Db    421 ATATATGTACCTACCTCCTTATGAAGTATTACTATGTCGATCGTTAACAATTCTCAATAT 480

Qy     97 ---------------------------------------------------------- 97

Db    481 CTTTAAACGCTTCTCCCTCTTTAGTTTCTTTCTTAAATTAACCTAATTAAACAACCTACA 540

Qy     97 ---------------------------------------------------------- 97

Db    541 TATATATCATAAGATATACAAATATGTGTATGTTTTCATAATTAGCTTATGTATGTTTAA 600

Qy     98 --------------------AlaMetAlaAlaIleGlyGluLysGluTrpTyrPheTyr 110
                               |||||||||||||||||||||||||||||||||||||
Db    601 TCATAGATATATGTATATGCAGCTATGGCGGCGATAGGAGAGAAAGAGTGGTACTTCTAT 660

Qy    111 ValProArgAspArgLysTyrArgAsnGlyAspArgProAsnArgValThrThrSerGly 130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTGCCAAGAGATCGGAAATATAGAAATGGAGATAGACCGAACCGAGTAACGACTTCAGGA 720

Qy    131 TyrTrpLysAlaThrGlyAlaAspArgMetIleArgSerGluThrSerArgProIleGly 150
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TATTGGAAAGCCACCGGAGCTGATAGGATGATCAGATCGGAGACTTCTCGGCCTATCGGA 780

Qy    151 LeuLysLysThrLeuValPheTyrSerGlyLysAlaProLysGlyThrArgThrSerTrp 170
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TTAAAGAAACCCTAGTTTTCTACTCTGGTAAAGCCCCTAAAGGCACTCGTACTAGTTGG 840

Qy    171 IleMetAsnGluTyrArgLeuProHisHisGluThrGluLysTyrGlnLysAla------ 188
              ||||||||||||||||||||||||||||||||||||||||||||.|||||||||||||
Db    841 ATCATGAACGAGTATCGTCTTCCGCACCATGAAACCGAGAAGTACCAAAAGGT-ATAAAT 899

Qy    188 ---------------------------------------------------------- 188
                                                          892-894
Db    900 TCTACTATAACTCTATATATATCCTATTCATACATACATAGATATAACCCTAGCTAGGTG 959

Qy    188 ---------------------------------------------------------- 188

Db    960 GTGAGGCCTTTAAAATTGAAATTAATCCCTAGACAGTTTGAATTTTTTCTTTTTTGACTA 1019

Qy    188 ---------------------------------------------------------- 188

Db   1020 GTTTTATTTATTTATTTTGGAATTGATTCGATAAGATCAAAAATACTTGTGAATGGACTA 1079

Qy    188 ---------------------------------------------------------- 188

Db   1080 AATGTCAGGCGGCGTTTGCGCTTAAATCCAGAAAAATGTTCATGTCATATGCGTGAACTC 1139

Qy    188 ---------------------------------------------------------- 188

Db   1140 TTTAAATTGCTAGACATGGCCCATATGTTATAGTAGAATACATTAATAGATAGATGCATA 1199

Qy    188 ---------------------------------------------------------- 188

Db   1200 CACATATATATAAACACACAAGTATCACACTCGACATTCATATACCTTAATTCTGCAGAG 1259
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Qy      188 ---------------------------------------------------------- 188

Db     1260 ACATAGTTAGTTTTTCTTACAATTTATGACATGAATGTTCCTGCTCTTCCTCACATTAAT 1319

Qy      188 ---------------------------------------------------------- 188

Db     1320 TCATGTCTTCTATTTAAGTTACCCAACATTTTTTGAAATAATTTGGCATATATGAATTAT 1379

Qy      188 ---------------------------------------------------------- 188

Db     1380 ACCAACATATTTATATGCGAACATTTAAAATCTATACGAATGATAACGGTTTATGGAGTA 1439

Qy      188 ---------------------------------------------------------- 188

Db     1440 GACCGAAAAAATATTATGTATACGGAAAATGACAATGGATAGATAAATACATTTTTTGGG 1499

Qy      188 ---------------------------------------------------------- 188

Db     1500 CTCTTTCGACTTATATGTCGTCACCATTTGAAACCATAAATTTATAAAATTTTCTATGTA 1559

Qy      188 ---------------------------------------------------------- 188

Db     1560 TATATATGATATTATGATGTATGCATAAGACAGCTAAAACAACAGGGTTGACATAATTAT 1619

Qy      188 ---------------------------------------------------------- 188

Db     1620 CTATGTGTATGTATTGCACATTCACTTGTACTAATAAAACTAAAATTACGCAATTAAATA 1679

Qy      188 ---------------------------------------------------------- 188

Db     1680 TATAAAAAATAATAAATATAATCATCTTAATTATATTTGCATTGTTACGTCATATGATAG 1739

Qy      188 ---------------------------------------------------------- 188

Db     1740 TACTCTAAATTTCTTCTAAACGTGCTATCTTTTTTTGCTAATGCTAACTTTACATAGTTT 1799

Qy      188 ---------------------------------------------------------- 188

Db     1800 GTGAATCTTCTTTCAAAACCATATCTTCGATAAATGATATTTTTCATAGATATTGTTAGT 1859

Qy      188 ---------------------------------------------------------- 188

Db     1860 CTATATTTGATAATTTGATATATGTATCAAGTCTCTAATCAATGTGCTCATGTATAATTA 1919

Qy      189 ------GluIleSerLeuCysArgValTyrLysArgProGlyValGluAspHisProSer 206
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1920 TAGGCTGAAATATCATTGTGCCGAGTGTACAAAAGGCCAGGAGTAGAAGATCATCCATCG 1979

Qy      207 ValProArgSerLeuSerThrArgHisHisAsnHisAsnSerSerThrSerSerArgLeu 226
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1980 GTACCACGTTCTCTCTCCACAAGACATCATAACCATAACTCATCGACATCATCCCGTTTA 2039

Qy      227 AlaLeuArgGlnGlnGlnHisHisSerSerSerSerAsnHisSerAspAsnAsnLeuAsn 246
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2040 GCCTTAAGACAACAACAACACCATTCATCCTCCTCTAATCATTCCGACAACAACCTTAAC 2099

Qy      247 AsnAsnAsnAsnIleAsnAsnLeuGluLysLeuSerThrGluTyrSerGlyAspGlySer 266
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2100 AACAACAACAACATCAACAATCTCGAGAAGCTCTCCACCGAATATTCCGGCGACGGCAGC 2159
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Qy      267 ThrThrThrThrThrThrAsnSerAsnSerAspValThrIleAlaLeuAlaAsnGlnAsn 286
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2160 ACAACAACAACGACCACAAACAGTAACTCTGACGTTACCATTGCTCTAGCCAATCAAAAC 2219

Qy      287 IleTyrArgProMetProTyrAspThrSerAsnAsnThrLeuIleValSerThrArgAsn 306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2220 ATATATCGTCCAATGCCTTACGACACAAGCAACAACACATTGATAGTCTCTACGAGAAAT 2279

Qy      307 HisGlnAspAspAspGluThrAlaIleValAspAspLeuGlnArgLeuValAsnTyrGln 326
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2280 CATCAAGACGATGATGAAACTGCCATTGTTGACGATCTTCAAAGACTAGTTAACTACCAA 2339

Qy      327 IleSerAspGly------------------------------------------------ 330
            ||||||||||||
Db     2340 ATATCAGATGGAGGTAACATCAATCACCAATACTTTCAAATTGCTCAACAGTTTCATCAT 2399

Qy      331 --------------------------------------------------------Ala 331
                                                                     |||
Db     2400 ACTCAACAACAAAATGCTAACGCAAACGCATTACAATTGGTGGCTGCGGCGACTACAGCG 2459

Qy      332 ThrThrLeuMetProGlnThrGlnAlaAlaLeuAlaMetAsnMetIleProAlaGlyThr 351
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2460 ACAACGCTAATGCCTCAAACTCAAGCGGCGTTAGCTATGAACATGATTCCTGCAGGAACG 2519

Qy      352 IleProAsnAsnAlaLeuTrpAspMetTrpAsnProIleValProAspGlyAsnArgAsp 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2520 ATTCCAAACAATGCTTTGTGGGATATGTGGAATCCAATAGTACCAGATGGAAACAGAGAT 2579

Qy      372 HisTyrThrAsnIleProPheLys 379
            ||||||||||||||||||||||||
Db     2580 CACTATACTAATATTCCTTTTAAG 2603
```